



PCT10

RAW SEQUENCE LISTING

DATE: 06/25/2003

PATENT APPLICATION: US/09/857,855

TIME: 09:30:09

Input Set : A:\A-574.app

Output Set: N:\CRF4\06252003\I857855.raw

3 <110> APPLICANT: Simonet, William S.
 4 Asuncion, Franklin J.
 5 Min, Hosung
 6 Jing, Shuqian
 8 <120> TITLE OF INVENTION: GRNF4 A Neurotrophic Factor
 10 <130> FILE REFERENCE: A-574PCT
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/857,855
 C--> 13 <141> CURRENT FILING DATE: 2003-05-06
 15 <150> PRIOR APPLICATION NUMBER: 60/111,626
 16 <151> PRIOR FILING DATE: 1998-12-09
 18 <160> NUMBER OF SEQ ID NOS: 12
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 378
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Murine
 27 <220> FEATURE: *pp 1-2*
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (2)..(376)
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: The amino acid Xaa in position #79 may be proline.
 33 The amino acid Xaa in position #102 may be
 34 tryptophan. The amino acid Xaa in position #118
 35 and #120 can be any amino acid.
 37 <400> SEQUENCE: 1
 38 c gcg tgg gcg cgt gca gga acc cgg agc agc cgc gca cgg acc aca gat 49
 39 Ala Trp Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp
 40 1 5 10 15
 42 gcg cgc ggc tgc cgc ctg cgc tcg cag ctg gtg ccg gtg agt gcg ctc 97
 43 Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu
 44 20 25 30
 46 ggc cta ggc cac agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc 145
 47 Gly Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser
 48 35 40 45
 50 ggc tcg tgc cgt cga gca cgc tcc cag cac gat ctc agt ctg gcc agc 193
 51 Gly Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser
 52 50 55 60
 W--> 54 cta ctg ggc gct ggg gcc cta cgg tcg cct ccc ggg tcc cgg *ncg* atc 241
 55 Leu Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Xaa Ile
 56 65 70 75 80
 58 agc cag ccc tgc tgc cgg ccc act cgc tat gag gcc gtc tcc ttc atg 289
 59 Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met
 60 85 90 95

pp 1-4, 6
Does Not Comply
Corrected Diskette Needed

see p. 6 for error explanation

*since this
 is a nucleotide
 sequence, all
 n's have to be
 explained*

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```

62 gac gtg aac agc acc tgg agg acc gtg gac cac ctc tcc gcc act gcc 337
63 Asp Val Asn Ser Thr Xaa Arg Thr Val Asp His Leu Ser Ala Thr Ala
64 100 105 110
66 tgc ggc tgt ctg ggc nnn gga nnn tct atc tcc aag cct tt 378
67 Cys Gly Cys Leu Gly Xaa Gly Xaa Ser Ile Ser Lys Pro
68 115 120 125

```

71 <210> SEQ ID NO: 2

72 <211> LENGTH: 125

73 <212> TYPE: PRT

74 <213> ORGANISM: Murine

75 <223> OTHER INFORMATION: The amino acid Xaa in position #79 may be proline.

76 The amino acid Xaa in position #102 may be

77 tryptophan. The amino acid Xaa in position #118

78 and #120 can be any amino acid.

80 <400> SEQUENCE: 2

81 Ala Trp Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp

82 1 5 10 15

84 Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu

85 20 25 30

87 Gly Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser

88 35 40 45

90 Gly Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser

91 50 55 60

W--> 93 Leu Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Xaa Ile

94 65 70 75 80

96 Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met

97 85 90 95

99 Asp Val Asn Ser Thr Xaa Arg Thr Val Asp His Leu Ser Ala Thr Ala

100 100 105 110

102 Cys Gly Cys Leu Gly Xaa Gly Xaa Ser Ile Ser Lys Pro

103 115 120 125

107 <210> SEQ ID NO: 3

108 <211> LENGTH: 143

109 <212> TYPE: PRT

110 <213> ORGANISM: Murine

112 <220> FEATURE:

113 <223> OTHER INFORMATION: neurturin mouse

115 <400> SEQUENCE: 3

116 Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala Pro Asp Ala Val

117 1 5 10 15

119 Glu Leu Arg Glu Leu Ser Pro Trp Ala Ala Arg Ile Pro Gly Pro Arg

120 20 25 30

122 Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Pro Gly Ala Arg Pro

123 35 40 45

125 Cys Gly Leu Arg Glu Leu Glu Val Arg Val Ser Glu Leu Gly Leu Gly

126 50 55 60

128 Tyr Thr Ser Asp Glu Thr Val Leu Phe Arg Tyr Cys Ala Gly Ala Cys

129 65 70 75 80

131 Glu Ala Ala Ile Arg Ile Tyr Asp Leu Gly Leu Arg Arg Leu Arg Gln

><220> insert this mandatory

remove identifier wherever

<221>, <222>, or <223> is shown

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```

132          85          90          95
134 Arg Arg Arg Val Arg Arg Glu Arg Ala Arg Ala His Pro Cys Cys Arg
135          100          105          110
137 Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe Leu Asp Val His Ser Arg
138          115          120          125
140 Tyr His Thr Leu Gln Glu Leu Ser Ala Arg Glu Cys Ala Cys Val
141          130          135          140
144 <210> SEQ ID NO: 4
145 <211> LENGTH: 1054
146 <212> TYPE: DNA
147 <213> ORGANISM: Murine
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (18)..(1052)
153 <220> FEATURE:
154 <223> OTHER INFORMATION: The amino acid Xaa in any position can be any
155 amino acid
157 <400> SEQUENCE: 4
158 cggacgcgtg ggcggac gcg tgg gcg cgt gca gga acc cgg agc agc cgc 50
159          Ala Trp Ala Arg Ala Gly Thr Arg Ser Ser Arg
160          1          5          10
162 gca cgg acc aca gat gcg cgc ggc tgc cgc ctg cgc tcg cag ctg gtg 98
163 Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val
164          15          20          25
166 ccg gtg agt gcg ctc ggc cta ggc cac agc tcc gac gag ctg ata cgt 146
167 Pro Val Ser Ala Leu Gly Leu Gly His Ser Ser Asp Glu Leu Ile Arg
168          30          35          40
170 ttc cgc ttc tgc agc ggc tcg tgc cgc cga gca cgc tcc cag cac gat 194
171 Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Gln His Asp
172          45          50          55
174 ctc agt ctg gcc agc cta ctg ggc gct ggg gcc cta cgg tcg cct ccc 242
175 Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro
176 60          65          70          75
178 ggg tcc cgg ccg atc agc cag ccc tgc tgc cgg ccc act cgc tat gag 290
179 Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu
180          80          85          90
182 gcc gtc tcc ttc atg gac gtg aac agc acc tgg agg acc gtg gac cac 338
183 Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp His
184          95          100          105
W--> 186 ctc tcc gcc act gcc tgc ggc tgt ctg ggc nnn gga nnn tct atc tcc 386
187 Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly Xaa Gly Xaa Ser Ile Ser
188          110          115          120
190 aag cct ttg cac act aga ccc atg tgt tgc cct acc tgg aac agc tcc 434
191 Lys Pro Leu His Thr Arg Pro Met Cys Cys Pro Thr Trp Asn Ser Ser
192          125          130          135
194 acc ggg cct cac nnn cca gga gcc tca act cag cag gat atg gag gct 482
195 Thr Gly Pro His Xaa Pro Gly Ala Ser Thr Gln Gln Asp Met Glu Ala
196 140          145          150          155
198 gca gag ctc agg ccc cag gcc ggt gag nnn cag acg tcg tcg gca nnn 530

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DATE: 06/25/2003

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Input Set : A:\A-574.app

Output Set: N:\CRF4\06252003\I857855.raw

```

199 Ala Glu Leu Arg Pro Gln Ala Gly Glu Xaa Gln Thr Ser Ser Ala Xaa
200                               160                               165                               170
202 cag aca gag (nnn) aag atg tgc gaa cca ctg acc aac agt ccc aag ttg 578
203 Gln Thr Glu Xaa Lys Met Ser Glu Pro Leu Thr Asn Ser Pro Lys Leu
204                               175                               180                               185
206 ttc atg gat cac agc tct aca gac agg aga aac ctc agc (nnn) aga gaa 626
207 Phe Met Asp His Ser Ser Thr Asp Arg Arg Asn Leu Ser Xaa Arg Glu
208                               190                               195                               200
210 ctc ctc tgg gag aat cca gaa atg gcc ctc tgt cct ggg gaa (nnn) att 674
211 Leu Leu Trp Glu Asn Pro Glu Met Ala Leu Cys Pro Gly Glu Xaa Ile
212                               205                               210                               215
214 ttg aag aga tat ata tac ata tat aca ttg (nnn) tgc cgt tgc tgg acc 722
215 Leu Lys Arg Tyr Ile Tyr Ile Tyr Thr Leu Xaa Ser Arg Cys Trp Thr
216 220                               225                               230                               235
218 agc ctg tgc (nnn) aac cag tcc cgt gtt cac ttg tgg aag ccg aag ccc 770
219 Ser Leu Cys Xaa Asn Gln Ser Arg Val His Leu Trp Lys Pro Lys Pro
220                               240                               245                               250
222 tat tta tta ttt cta aat tat tta ttt act ttg ctg gtt tgt cag atc 818
223 Tyr Leu Leu Phe Leu Asn Tyr Leu Phe Thr Leu Leu Val Cys Gln Ile
224                               255                               260                               265
226 ctt tcc tgg aca tgg ggg atg gta gaa gaa gct aga (nnn) aga tgt gcc 866
227 Leu Ser Trp Thr Trp Gly Met Val Glu Glu Ala Arg Xaa Arg Cys Ala
228                               270                               275                               280
230 cca ccc cac ccc ccc atc cac att tta cac ttg act cag (nnn) tgc tac 914
231 Pro Pro His Pro Pro Ile His Ile Leu His Leu Thr Gln Xaa Cys Tyr
232                               285                               290                               295
234 ctg gat cgc cta ctt ctt gcc ccg cag gtg tct ctg aga tgg atg gga 962
235 Leu Asp Arg Leu Leu Leu Ala Pro Gln Val Ser Leu Arg Trp Met Gly
236 300                               305                               310                               315
238 ggc aca cat agg (nnn) caa aga tgc aca atc cac agt act tgg ggc ctg 1010
239 Gly Thr His Arg Xaa Gln Arg Cys Thr Ile His Ser Thr Trp Gly Leu
240                               320                               325                               330
242 ggg tac cta tgg gaa ata aac aat ata gtt ttc tat gga aaa aa 1054
243 Gly Tyr Leu Trp Glu Ile Asn Asn Ile Val Phe Tyr Gly Lys
244                               335                               340                               345
247 <210> SEQ ID NO: 5
248 <211> LENGTH: 345
249 <212> TYPE: PRT
250 <213> ORGANISM: Murine
251 <223> OTHER INFORMATION: The amino acid Xaa in any position can be any
252 amino acid
254 <400> SEQUENCE: 5
255 Ala Trp Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp
256 1 5 10 15
258 Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu
259 20 25 30
261 Gly Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser
262 35 40 45
264 Gly Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser

```

Please
see p. 6
to ensure
that
all n's or
Xaa's
are
explained
in their
appropriate
sequences.

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TIME: 09:30:09

Input Set : A:\A-574.app

Output Set: N:\CRF4\06252003\I857855.raw

```

265      50      55      60
267 Leu Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile
268 65      70      75      80
270 Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met
271      85      90      95
273 Asp Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala
274      100      105      110
W--> 276 Cys Gly Cys Leu Gly Xaa Gly Xaa Ser Ile Ser Lys Pro Leu His Thr
277      115      120      125
279 Arg Pro Met Cys Cys Pro Thr Trp Asn Ser Ser Thr Gly Pro His Xaa
280      130      135      140
282 Pro Gly Ala Ser Thr Gln Gln Asp Met Glu Ala Ala Glu Leu Arg Pro
283 145      150      155      160
285 Gln Ala Gly Glu Xaa Gln Thr Ser Ser Ala Xaa Gln Thr Glu Xaa Lys
286      165      170      175
288 Met Ser Glu Pro Leu Thr Asn Ser Pro Lys Leu Phe Met Asp His Ser
289      180      185      190
291 Ser Thr Asp Arg Arg Asn Leu Ser Xaa Arg Glu Leu Leu Trp Glu Asn
292      195      200      205
294 Pro Glu Met Ala Leu Cys Pro Gly Glu Xaa Ile Leu Lys Arg Tyr Ile
295      210      215      220
297 Tyr Ile Tyr Thr Leu Xaa Ser Arg Cys Trp Thr Ser Leu Cys Xaa Asn
298 225      230      235      240
300 Gln Ser Arg Val His Leu Trp Lys Pro Lys Pro Tyr Leu Leu Phe Leu
301      245      250      255
303 Asn Tyr Leu Phe Thr Leu Leu Val Cys Gln Ile Leu Ser Trp Thr Trp
304      260      265      270
306 Gly Met Val Glu Glu Ala Arg Xaa Arg Cys Ala Pro Pro His Pro Pro
307      275      280      285
309 Ile His Ile Leu His Leu Thr Gln Xaa Cys Tyr Leu Asp Arg Leu Leu
310      290      295      300
312 Leu Ala Pro Gln Val Ser Leu Arg Trp Met Gly Gly Thr His Arg Xaa
313 305      310      315      320
315 Gln Arg Cys Thr Ile His Ser Thr Trp Gly Leu Gly Tyr Leu Trp Glu
316      325      330      335
318 Ile Asn Asn Ile Val Phe Tyr Gly Lys
319      340      345
323 <210> SEQ ID NO: 6
324 <211> LENGTH: 1013
325 <212> TYPE: DNA
326 <213> ORGANISM: Murine
328 <220> FEATURE:
329 <221> NAME/KEY: CDS
330 <222> LOCATION: (217)..(891)
332 <400> SEQUENCE: 6
333 ccaagcttgg taccgagctc ggatccacta gtaacggccg ccagtgtgct ggaattcgcc 60
335 ctactact atagggctcg agcggccgcc cgggcaggta taaaaaaaaa aagcggccta 120
337 gaattcagcg gccgctgaat tctaggctgc cgcaggaaga ggggtgggaa acgggtccac 180
339 gaaggcttct gatgggagct tctggagccg aaagct atg gaa ctg gga ctt gca 234

```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/857,855

DATE: 06/25/2003
TIME: 09:30:11

Input Set : A:\A-574.app

Output Set: N:\CRF4\06252003\I857855.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. ~~236, 307, 353, 354, 355, 359, 360, 361~~

Seq#:1; Xaa Pos. ~~78, 102, 118, 120~~

Seq#:2; Xaa Pos. ~~79, 102, 118, 120~~

Seq#:4; N Pos. ~~369, 370, 371, 375, 376, 377, 447, 448, 449, 510, 511, 512, 528, 529, 530~~

Seq#:4; N Pos. ~~540, 541, 542, 618, 619, 620, 669, 670, 671, 705, 706, 707, 732, 733, 734~~

Seq#:4; N Pos. ~~855, 856, 857, 906, 907, 908, 975, 976, 977~~

Seq#:4; Xaa Pos. 118, 120, 144, 165, 171, 175, 201, 218, 230, 239, 280, 297, 320

Seq#:5; Xaa Pos. 118, 120, 144, 165, 171, 175, 201, 218, 230, 239, 280, 297, 320

Seq#:12; Xaa Pos. 6, 7, 8, 9, 10, 15, 16, 19, 20, 21, 22, 23, 24, 25, 26, 27, 29, 31, 37, 43

Seq#:12; Xaa Pos. 45, 50, 51, 52, 53, 58, 60, 63, 68, 70, 71, 77, 80, 81, 84, 86, 87, 93, 94

Seq#:12; Xaa Pos. 95, 102, 104, 105, 106, 107, 109, 110, 111, 112, 115, 122, 123, 124

Seq#:12; Xaa Pos. 129, 130, 131, 145, 152, 157, 172, 188, 195, 222